

## SEQUENCE LISTING

<110> Glucksmann, Maria Alexandra  
Meyers, Rachel  
Rudolph-Owen, Laura A.

<120> NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

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Pro Phe Thr Met Phe Phe Ser Val His Asp Pro Asp Tyr Ala Lys Ile
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 ggggagcggg ggaggcagct gaggaagttt accatgcttg ctctgcggga cctgggcatg 420  
 gggaagcag agggcgagga gctgatccag gcggaggccc ggtgtctggt ggagacattc 480  
 caggggacag aaggacgccc attcgatccc tcctgctgc tggcccaggc cacctccaac 540  
 gtagtctgct cctcctctt tggcctccgc ttctcctatg aggataagga gttccaggcc 600  
 gtggtccggg cagctggtgg taccctgctg ggagtcagct ccagggggg tcagacctac 660  
 gagatgttct cctggttctt gcggcccctg ccaggccccc acaagcagct cctccaccac 720  
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 caaaaccag gcacagaatt caccaacaag aacatgctga tgacagtcac ttatttgctg 900  
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 catgaccca acatcttcaa gcaccagaa gagttcaacc cagaccgttt cctggatgca 1260  
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<210> 7  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
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 ccgcgcgcgc ccggacc atg tcg tct ccg ggg ccg tcg cag ccg ccg gcc 110  
                                  Met Ser Ser Pro Gly Pro Ser Gln Pro Pro Ala  
                                  1                      5                      10  
 gag gac ccg ccc tgg ccc gcg cgc ctc ctg cgt gcg cct ctg ggg ctg 158  
 Glu Asp Pro Pro Trp Pro Ala Arg Leu Leu Arg Ala Pro Leu Gly Leu  
                                  15                      20                      25

ctg cgg ctg gac ccc agc ggg ggc gcg ctg ctg cta tgc ggc ctc gta Leu Arg Leu Asp Pro Ser Gly Gly Ala Leu Leu Leu Cys Gly Leu Val 30 35 40	206
gcg ctg ctg ggc tgg agc tgg ctg cgg agg cgc cgg gcg cgg ggc atc Ala Leu Leu Gly Trp Ser Trp Leu Arg Arg Arg Arg Ala Arg Gly Ile 45 50 55	254
ccg ccc ggg ccc acg ccc tgg cct ctg gtg ggc aac ttc ggt cac gtg Pro Pro Gly Pro Thr Pro Trp Pro Leu Val Gly Asn Phe Gly His Val 60 65 70 75	302
ctg ctg cct ccc ttc ctc cgg cgg cgg agc tgg ctg agc agc agg acc Leu Leu Pro Pro Phe Leu Arg Arg Arg Ser Trp Leu Ser Ser Arg Thr 80 85 90	350
agg gcc gca ggg att gat ccc tcg gtc ata ggc ccg cag gtg ctc ctg Arg Ala Ala Gly Ile Asp Pro Ser Val Ile Gly Pro Gln Val Leu Leu 95 100 105	398
gct cac cta gcc cgc gtg tac ggc agc atc ttc agc ttc ttt atc ggc Ala His Leu Ala Arg Val Tyr Gly Ser Ile Phe Ser Phe Phe Ile Gly 110 115 120	446
cac tac ctg gtg gtg gtc ctc agc gac ttc cac agc gtg cgc gag gcg His Tyr Leu Val Val Val Leu Ser Asp Phe His Ser Val Arg Glu Ala 125 130 135	494
ctg gtg cag cag gcc gag gtc ttc agc gac cgc ccg cgg gtg ccg ctc Leu Val Gln Gln Ala Glu Val Phe Ser Asp Arg Pro Arg Val Pro Leu 140 145 150 155	542
atc tcc atc gtg acc aag gag aag ggg gtt gtg ttt gca cat tat ggt Ile Ser Ile Val Thr Lys Glu Lys Gly Val Val Phe Ala His Tyr Gly 160 165 170	590
ccc gtc tgg aga caa caa agg aag ttc tct cat tca act ctt cgt cat Pro Val Trp Arg Gln Gln Arg Lys Phe Ser His Ser Thr Leu Arg His 175 180 185	638
ttt ggg ttg gga aaa ctt agc ttg gag ccc aag att att gag gag ttc Phe Gly Leu Gly Lys Leu Ser Leu Glu Pro Lys Ile Ile Glu Glu Phe 190 195 200	686
aaa tat gtg aaa gca gaa atg caa aag cac gga gaa gac ccc ttc tgc Lys Tyr Val Lys Ala Glu Met Gln Lys His Gly Glu Asp Pro Phe Cys 205 210 215	734
cct ttc tcc atc atc agc aat gcc gtc tct aac atc att tgc tcc ttg Pro Phe Ser Ile Ile Ser Asn Ala Val Ser Asn Ile Ile Cys Ser Leu 220 225 230 235	782
tgc ttt ggc cag cgc ttt gat tac act aat agt gag ttc aag aaa atg Cys Phe Gly Gln Arg Phe Asp Tyr Thr Asn Ser Glu Phe Lys Lys Met 240 245 250	830

ctt ggt ttt atg tca cga ggc cta gaa atc tgt ctg aac agt caa gtc Leu Gly Phe Met Ser Arg Gly Leu Glu Ile Cys Leu Asn Ser Gln Val 255 260 265	878
ctc ctg gtc aac ata tgc cct tgg ctt tat tac ctt ccc ttt gga cca Leu Leu Val Asn Ile Cys Pro Trp Leu Tyr Tyr Leu Pro Phe Gly Pro 270 275 280	926
ttt aag gaa tta aga caa att gaa aag gat ata acc agt ttc ctt aaa Phe Lys Glu Leu Arg Gln Ile Glu Lys Asp Ile Thr Ser Phe Leu Lys 285 290 295	974
aaa atc atc aaa gac cat caa gag tct ctg gat aga gag aac cct cag Lys Ile Ile Lys Asp His Gln Glu Ser Leu Asp Arg Glu Asn Pro Gln 300 305 310 315	1022
gac ttc ata gac atg tac ctt ctc cac atg gaa gag gag agg aaa aat Asp Phe Ile Asp Met Tyr Leu Leu His Met Glu Glu Glu Arg Lys Asn 320 325 330	1070
aat agt aac agc agt ttt gat gaa gag tac tta ttt tat atc att ggg Asn Ser Asn Ser Ser Phe Asp Glu Glu Tyr Leu Phe Tyr Ile Ile Gly 335 340 345	1118
gat ctc ttt att gct ggg act gat acc aca act aac tct ttg ctc tgg Asp Leu Phe Ile Ala Gly Thr Asp Thr Thr Thr Asn Ser Leu Leu Trp 350 355 360	1166
tgc ctg ctg tat atg tcg ctg aac ccc gat gta caa gaa aag gtt cat Cys Leu Leu Tyr Met Ser Leu Asn Pro Asp Val Gln Glu Lys Val His 365 370 375	1214
gaa gaa att gaa aga gtc att ggc gcc aac cga gct cct tcc ctc aca Glu Glu Ile Glu Arg Val Ile Gly Ala Asn Arg Ala Pro Ser Leu Thr 380 385 390 395	1262
gac aag gcc cag atg ccc tac aca gaa gcc acc atc atg gaa gtg cag Asp Lys Ala Gln Met Pro Tyr Thr Glu Ala Thr Ile Met Glu Val Gln 400 405 410	1310
agg cta act gtg gtg gtg ccg ctt gcc att cct cat atg acc tca gag Arg Leu Thr Val Val Val Pro Leu Ala Ile Pro His Met Thr Ser Glu 415 420 425	1358
aac aca gtg ctc caa ggg tat acc att cct aaa ggc aca ttg atc tta Asn Thr Val Leu Gln Gly Tyr Thr Ile Pro Lys Gly Thr Leu Ile Leu 430 435 440	1406
ccc aac ctg tgg tca gta cat aga gac cca gcc att tgg gag aaa ccg Pro Asn Leu Trp Ser Val His Arg Asp Pro Ala Ile Trp Glu Lys Pro 445 450 455	1454
gag gat ttc tac cct aat cga ttt ctg gat gac caa gga caa cta att Glu Asp Phe Tyr Pro Asn Arg Phe Leu Asp Asp Gln Gly Gln Leu Ile 460 465 470 475	1502
aaa aaa gaa acc ttt att cct ttt ggg ata ggg aag cgg gtg tgt atg	1550

Lys Lys Glu Thr Phe Ile Pro Phe Gly Ile Gly Lys Arg Val Cys Met  
 480 485 490

gga gaa caa ctg gca aag atg gaa tta ttc cta atg ttt gtg agc cta 1598  
 Gly Glu Gln Leu Ala Lys Met Glu Leu Phe Leu Met Phe Val Ser Leu  
 495 500 505

atg cag agt ttc gca ttt gct tta cct gag gat tct aag aag ccc ctc 1646  
 Met Gln Ser Phe Ala Phe Ala Leu Pro Glu Asp Ser Lys Lys Pro Leu  
 510 515 520

ctg act gga aga ttt ggt cta act tta gcc cca cat cca ttt aat ata 1694  
 Leu Thr Gly Arg Phe Gly Leu Thr Leu Ala Pro His Pro Phe Asn Ile  
 525 530 535

act att tca agg aga tgaagagcat ctccaagaag agatggtaaa aagatatata 1749  
 Thr Ile Ser Arg Arg  
 540

aatacatatc cttctaagca gattcttctt actgcaaagg acagtgaatc cagcaactca 1809  
 gtggatccaa gctgggctca gaggtcggaa ggagggtaga gcacactggg aggtttcatc 1869  
 ttggaggatt cctcagcagg atacttcagc catttttagta atgcaggtct gtgatttggg 1929  
 ggatagaaaa caaagtacct atgaaacggg atatctggat tttacttgca gtggcttcca 1989  
 ccgatgggcc aatcttctca tttcttagtg cctcagacat cccatatgta aaatgagagt 2049  
 aataaaactt ggcttctctc taaaaaaaa mamtaaaaaa aaaaaaaaaa 2099

<210> 8  
 <211> 544  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
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 Pro Ala Arg Leu Leu Arg Ala Pro Leu Gly Leu Leu Arg Leu Asp Pro  
 20 25 30  
 Ser Gly Gly Ala Leu Leu Leu Cys Gly Leu Val Ala Leu Leu Gly Trp  
 35 40 45  
 Ser Trp Leu Arg Arg Arg Arg Ala Arg Gly Ile Pro Pro Gly Pro Thr  
 50 55 60  
 Pro Trp Pro Leu Val Gly Asn Phe Gly His Val Leu Leu Pro Pro Phe  
 65 70 75 80  
 Leu Arg Arg Arg Ser Trp Leu Ser Ser Arg Thr Arg Ala Ala Gly Ile  
 85 90 95  
 Asp Pro Ser Val Ile Gly Pro Gln Val Leu Leu Ala His Leu Ala Arg  
 100 105 110  
 Val Tyr Gly Ser Ile Phe Ser Phe Phe Ile Gly His Tyr Leu Val Val  
 115 120 125  
 Val Leu Ser Asp Phe His Ser Val Arg Glu Ala Leu Val Gln Gln Ala  
 130 135 140  
 Glu Val Phe Ser Asp Arg Pro Arg Val Pro Leu Ile Ser Ile Val Thr  
 145 150 155 160  
 Lys Glu Lys Gly Val Val Phe Ala His Tyr Gly Pro Val Trp Arg Gln  
 165 170 175  
 Gln Arg Lys Phe Ser His Ser Thr Leu Arg His Phe Gly Leu Gly Lys  
 180 185 190  
 Leu Ser Leu Glu Pro Lys Ile Ile Glu Glu Phe Lys Tyr Val Lys Ala

195	200	205
Glu Met Gln Lys His Gly	Glu Asp Pro Phe Cys	Pro Phe Ser Ile Ile
210	215	220
Ser Asn Ala Val Ser Asn	Ile Ile Cys Ser Leu	Cys Phe Gly Gln Arg
225	230	235
Phe Asp Tyr Thr Asn Ser	Glu Phe Lys Lys Met	Leu Gly Phe Met Ser
245	250	255
Arg Gly Leu Glu Ile Cys	Leu Asn Ser Gln Val	Leu Leu Val Asn Ile
260	265	270
Cys Pro Trp Leu Tyr Tyr	Leu Pro Phe Gly Pro	Phe Lys Glu Leu Arg
275	280	285
Gln Ile Glu Lys Asp Ile	Thr Ser Phe Leu Lys	Lys Ile Ile Lys Asp
290	295	300
His Gln Glu Ser Leu Asp	Arg Glu Asn Pro Gln	Asp Phe Ile Asp Met
305	310	315
Tyr Leu Leu His Met Glu	Glu Glu Glu Arg Lys	Asn Asn Ser Asn Ser
325	330	335
Phe Asp Glu Glu Tyr Leu	Phe Tyr Ile Ile Gly	Asp Leu Phe Ile Ala
340	345	350
Gly Thr Asp Thr Thr Thr	Asn Ser Leu Leu Trp	Cys Leu Leu Tyr Met
355	360	365
Ser Leu Asn Pro Asp Val	Gln Glu Lys Val His	Glu Glu Ile Glu Arg
370	375	380
Val Ile Gly Ala Asn Arg	Ala Pro Ser Leu Thr	Asp Lys Ala Gln Met
385	390	395
Pro Tyr Thr Glu Ala Thr	Ile Met Glu Val Gln	Arg Leu Thr Val Val
405	410	415
Val Pro Leu Ala Ile Pro	His Met Thr Ser Glu	Asn Thr Val Leu Gln
420	425	430
Gly Tyr Thr Ile Pro Lys	Gly Thr Leu Ile Leu	Pro Asn Leu Trp Ser
435	440	445
Val His Arg Asp Pro Ala	Ile Trp Glu Lys Pro	Glu Asp Phe Tyr Pro
450	455	460
Asn Arg Phe Leu Asp Asp	Gln Gly Gln Leu Ile	Lys Lys Glu Thr Phe
465	470	475
Ile Pro Phe Gly Ile Gly	Lys Arg Val Cys Met	Gly Glu Gln Leu Ala
485	490	495
Lys Met Glu Leu Phe Leu	Met Phe Val Ser Leu	Met Gln Ser Phe Ala
500	505	510
Phe Ala Leu Pro Glu Asp	Ser Lys Lys Pro Leu	Leu Thr Gly Arg Phe
515	520	525
Gly Leu Thr Leu Ala Pro	His Pro Phe Asn Ile	Thr Ile Ser Arg Arg
530	535	540

&lt;210&gt; 9

&lt;211&gt; 1635

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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ctgcgtgcgc	ctctggggct	gctgcggctg	gaccccagcg	ggggcgcgct	gctgctatgc	120
ggcctcgtag	cgtctgtggg	ctggagctgg	ctgcggaggc	gccgggcgcg	gggcatcccg	180
cccgggcccc	cgccctggcc	tctggtgggc	aacttcggtc	acgtgctgct	gcctcccttc	240
ctccggcggc	ggagctggct	gagcagcagg	accagggccg	cagggattga	tccctcggtc	300
ataggccccg	aggtgctcct	ggctcaccta	gcccgcgtgt	acggcagcat	cttcagcttc	360
tttatcggcc	actacctggt	ggtggtcctc	agcgacttcc	acagcgtgcg	cgaggcgctg	420

gtgcagcagg	ccgaggtctt	cagcgaccgc	ccgcgggtgc	cgctcatctc	catcgtgacc	480
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tctcattcaa	ctcttcgtca	ttttgggttg	ggaaaactta	gcttgagacc	caagattatt	600
gaggagttca	aatatgtgaa	agcagaaatg	caaaagcacg	gagaagaccc	cttctgccct	660
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atctgtctga	acagtcaagt	cctcctggtc	aacatatgcc	cttggcttta	ttaccttccc	840
tttgaccat	ttaaggaatt	aagacaaatt	gaaaaggata	taaccagttt	ccttaaaaaa	900
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gaaattgaaa	gagtcattgg	cgccaaccga	gctccttccc	tcacagacaa	ggcccagatg	1200
ccctacacag	aagccaccat	catggaagtg	cagaggctaa	ctgtgggtggt	gccgcttgcc	1260
attcctcata	tgacctcaga	gaacacagtg	ctccaagggt	ataccattcc	taaaggcaca	1320
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gatttctacc	ctaatcgatt	tctggatgac	caaggacaac	taattaaaaa	agaaaccttt	1440
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ttcctaattg	ttgtgagcct	aatgcagagt	ttcgcatttg	ctttacctga	ggattctaag	1560
aagcccctcc	tgactggaag	atttgggtcta	actttagccc	cacatccatt	taatataact	1620
atttcaagga	gatga					1635

&lt;210&gt; 10

&lt;211&gt; 496

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 10

Pro	Pro	Gly	Pro	Pro	Pro	Leu	Pro	Leu	Ile	Gly	Asn	Leu	Leu	Gln	Leu
1				5					10					15	
Gly	Arg	Ala	Pro	Gly	Pro	Ile	Pro	His	Ser	Leu	Thr	Lys	Leu	Arg	Lys
			20					25					30		
Ala	Lys	Arg	Tyr	Gly	Lys	Pro	Val	Phe	Thr	Leu	Tyr	Leu	Gly	Pro	Arg
		35					40					45			
Pro	Val	Val	Val	Leu	Thr	Gly	Pro	Glu	Ala	Val	Lys	Glu	Val	Leu	Ile
	50					55					60				
Asp	Lys	Gly	Glu	Glu	Phe	Ala	Lys	Gly	Arg	Gly	Asp	Phe	Asn	Pro	Thr
65					70					75				80	
Phe	Pro	Trp	Leu	Ser	Lys	Gly	Tyr	Arg	Glu	Gln	Gly	Leu	Leu	Phe	Ser
			85						90					95	
Asp	Asn	Gly	Pro	Lys	Trp	Arg	Lys	Leu	Arg	Arg	Phe	Ser	Leu	Leu	Thr
			100					105					110		
Leu	Arg	Phe	His	Phe	Gly	Met	Gly	Ala	Tyr	Ser	Lys	Arg	Ser	Gln	Lys
		115					120					125			
Leu	Glu	Glu	Pro	Arg	Ile	Gln	Glu	Glu	Ala	Arg	Asp	Leu	Val	Glu	Arg
	130					135					140				
Leu	Arg	Lys	Glu	Gln	Ala	Gly	Ser	Pro	Ile	Asp	Ile	Thr	Glu	Leu	Leu
145				150						155				160	
Ala	Arg	Leu	Ala	Pro	Leu	Asn	Val	Ile	Cys	Ser	Leu	Leu	Phe	Gly	Val
			165					170						175	
Arg	Phe	Asp	Tyr	Leu	Arg	Pro	Glu	Asp	Pro	Glu	Phe	Leu	Lys	Leu	Ile
			180					185					190		
Asp	Lys	Leu	Leu	Asn	Glu	Met	Phe	Asp	Arg	Val	Ser	Pro	Trp	His	Gln
		195				200						205			

```

Leu Leu Asp Ile Phe Pro Phe Leu Leu Arg Tyr Leu Pro Gly Ser Leu
 210                215                220
Phe Arg Lys Ala Phe Lys Ala Ala Lys Asp Leu Lys Asp Tyr Leu Asp
225                230                235                240
Lys Leu Ile Glu Glu Arg Arg Glu Thr Leu Glu Pro Ala Gly Asp Pro
                245                250                255
Arg Arg Leu Asp Ile Gly Phe Leu Asp Ser Leu Leu Leu Glu Ala Lys
                260                265                270
Arg Glu Gly Gly Asn Pro Lys Ser Glu Leu Ser Asp Glu Glu Leu Ala
                275                280                285
Ala Thr Val Leu Asp Leu Leu Phe Ala Gly Thr Glu Thr Thr Ser Ser
                290                295                300
Thr Leu Ser Trp Ala Leu Tyr Leu Leu Ala Lys His Pro Glu Val Gln
305                310                315                320
Ala Lys Leu Arg Glu Glu Ile Asp Glu Val Ile Gly Arg Asp Arg Ser
                325                330                335
Pro Thr Tyr Asp Val Asp Ala Arg Ala Gln Met Pro Tyr Leu Asp Ala
                340                345                350
Val Ile Lys Glu Thr Leu Arg Leu Tyr Pro Val Val Pro Leu Leu Leu
                355                360                365
Pro Arg Val Ala Thr Lys Asp Thr Glu Ile Pro Asp Gly Tyr Leu Ile
                370                375                380
Pro Lys Gly Thr Leu Val Ile Val Asn Leu Tyr Ser Leu His Arg Asp
385                390                395                400
Pro Lys Val Phe Pro Asn Pro Glu Glu Phe Asp Pro Glu Arg Phe Leu
                405                410                415
Asp Glu Asn Gly Lys Phe Lys Lys Ser Tyr Ala Phe Leu Pro Phe Gly
                420                425                430
Ala Gly Pro Arg Asn Cys Leu Gly Glu Arg Leu Ala Arg Met Glu Leu
                435                440                445
Phe Leu Phe Leu Ala Thr Leu Leu Gln Arg Phe Pro Glu Leu Glu Leu
                450                455                460
Ala Val Pro Pro Gly Asp Ile Pro Ser Leu Thr Pro Lys Pro Glu Leu
465                470                475                480
Gly Leu Pro Ser Lys Pro Pro Leu Tyr Lys Val Gln Leu Arg Pro Ala
                485                490                495

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<210> 11
<211> 13
<212> PRT
<213> Artificial Sequence

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<220>
<223> consensus sequence

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<400> 11
Pro Pro Gly Pro Pro Pro Leu Pro Leu Ile Gly Asn Leu
 1                5                10

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<210> 12
<211> 470
<212> PRT
<213> Artificial Sequence

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<220>
<223> consensus sequence

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&lt;400&gt; 12

Leu	Thr	Lys	Leu	Arg	Lys	Ala	Lys	Arg	Tyr	Gly	Lys	Pro	Val	Phe	Thr
1			5						10					15	
Leu	Tyr	Leu	Gly	Pro	Arg	Pro	Val	Val	Val	Leu	Thr	Gly	Pro	Glu	Ala
		20						25					30		
Val	Lys	Glu	Val	Leu	Ile	Asp	Lys	Gly	Glu	Glu	Phe	Ala	Lys	Gly	Arg
		35					40					45			
Gly	Asp	Phe	Asn	Pro	Thr	Phe	Pro	Trp	Leu	Ser	Lys	Gly	Tyr	Arg	Glu
	50					55					60				
Gln	Gly	Leu	Leu	Phe	Ser	Asp	Asn	Gly	Pro	Lys	Trp	Arg	Lys	Leu	Arg
65					70					75					80
Arg	Phe	Ser	Leu	Leu	Thr	Leu	Arg	Phe	His	Phe	Gly	Met	Gly	Ala	Tyr
			85						90					95	
Ser	Lys	Arg	Ser	Gln	Lys	Leu	Glu	Glu	Pro	Arg	Ile	Gln	Glu	Glu	Ala
			100					105					110		
Arg	Asp	Leu	Val	Glu	Arg	Leu	Arg	Lys	Glu	Gln	Ala	Gly	Ser	Pro	Ile
	115						120					125			
Asp	Ile	Thr	Glu	Leu	Leu	Ala	Arg	Leu	Ala	Pro	Leu	Asn	Val	Ile	Cys
	130					135					140				
Ser	Leu	Leu	Phe	Gly	Val	Arg	Phe	Asp	Tyr	Leu	Arg	Pro	Glu	Asp	Pro
145					150					155					160
Glu	Phe	Leu	Lys	Leu	Ile	Asp	Lys	Leu	Leu	Asn	Glu	Met	Phe	Asp	Arg
			165						170					175	
Val	Ser	Pro	Trp	His	Gln	Leu	Leu	Asp	Ile	Phe	Pro	Phe	Leu	Leu	Arg
			180					185					190		
Tyr	Leu	Pro	Gly	Ser	Leu	Phe	Arg	Lys	Ala	Phe	Lys	Ala	Ala	Lys	Asp
	195						200					205			
Leu	Lys	Asp	Tyr	Leu	Asp	Lys	Leu	Ile	Glu	Glu	Arg	Arg	Glu	Thr	Leu
	210					215					220				
Glu	Pro	Ala	Gly	Asp	Pro	Arg	Arg	Leu	Asp	Ile	Gly	Phe	Leu	Asp	Ser
225					230					235					240
Leu	Leu	Leu	Glu	Ala	Lys	Arg	Glu	Gly	Gly	Asn	Pro	Lys	Ser	Glu	Leu
			245						250					255	
Ser	Asp	Glu	Glu	Leu	Ala	Ala	Thr	Val	Leu	Asp	Leu	Leu	Phe	Ala	Gly
		260						265					270		
Thr	Glu	Thr	Thr	Ser	Ser	Thr	Leu	Ser	Trp	Ala	Leu	Tyr	Leu	Leu	Ala
		275					280						285		
Lys	His	Pro	Glu	Val	Gln	Ala	Lys	Leu	Arg	Glu	Glu	Ile	Asp	Glu	Val
	290					295					300				
Ile	Gly	Arg	Asp	Arg	Ser	Pro	Thr	Tyr	Asp	Val	Asp	Ala	Arg	Ala	Gln
305					310					315					320
Met	Pro	Tyr	Leu	Asp	Ala	Val	Ile	Lys	Glu	Thr	Leu	Arg	Leu	Tyr	Pro
			325						330					335	
Val	Val	Pro	Leu	Leu	Leu	Pro	Arg	Val	Ala	Thr	Lys	Asp	Thr	Glu	Ile
		340						345					350		
Pro	Asp	Gly	Tyr	Leu	Ile	Pro	Lys	Gly	Thr	Leu	Val	Ile	Val	Asn	Leu
	355						360					365			
Tyr	Ser	Leu	His	Arg	Asp	Pro	Lys	Val	Phe	Pro	Asn	Pro	Glu	Glu	Phe
	370					375					380				
Asp	Pro	Glu	Arg	Phe	Leu	Asp	Glu	Asn	Gly	Lys	Phe	Lys	Lys	Ser	Tyr
385					390					395					400
Ala	Phe	Leu	Pro	Phe	Gly	Ala	Gly	Pro	Arg	Asn	Cys	Leu	Gly	Glu	Arg
			405						410					415	
Leu	Ala	Arg	Met	Glu	Leu	Phe	Leu	Phe	Leu	Ala	Thr	Leu	Leu	Gln	Arg
		420						425					430		
Phe	Pro	Glu	Leu	Glu	Leu	Ala	Val	Pro	Pro	Gly	Asp	Ile	Pro	Ser	Leu
	435						440						445		

Thr Pro Lys Pro Glu Leu Gly Leu Pro Ser Lys Pro Pro Leu Tyr Lys  
 450 455 460  
 Val Gln Leu Arg Pro Ala  
 465 470

<210> 13  
 <211> 1043  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (175)...(885)

<400> 13  
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 ttggaagggg actccactc tctcctctt ttcgctgag tttgtgactc cgag atg 177  
 Met  
 1  
 gac aaa gtg tgt gct att ttt gga ggc tcc cga ggc att ggc agg gct 225  
 Asp Lys Val Cys Ala Ile Phe Gly Gly Ser Arg Gly Ile Gly Arg Ala  
 5 10 15  
 gtg gcc cag tta atg gcc cgg aaa ggc tac cgc ctg gcg atc att gcc 273  
 Val Ala Gln Leu Met Ala Arg Lys Gly Tyr Arg Leu Ala Ile Ile Ala  
 20 25 30  
 aga aac ctg gaa ggg gcc aaa gcc gcc gcc ggt gac ctc ggc gga gat 321  
 Arg Asn Leu Glu Gly Ala Lys Ala Ala Ala Gly Asp Leu Gly Gly Asp  
 35 40 45  
 cat ttg gca ttt agc tgt gat gtt gct aaa gaa cat gat gtt caa aat 369  
 His Leu Ala Phe Ser Cys Asp Val Ala Lys Glu His Asp Val Gln Asn  
 50 55 60 65  
 aca ttt gaa gag atg gag aaa cat tta ggt cga gta aat ttc ttg gta 417  
 Thr Phe Glu Glu Met Glu Lys His Leu Gly Arg Val Asn Phe Leu Val  
 70 75 80  
 aat gca gct ggt att aac agg gat agt ctt tta gta aga aca aaa act 465  
 Asn Ala Ala Gly Ile Asn Arg Asp Ser Leu Leu Val Arg Thr Lys Thr  
 85 90 95  
 gaa gat atg gta tct cag ctt cat act aac ctc ttg ggt tcc atg ctg 513  
 Glu Asp Met Val Ser Gln Leu His Thr Asn Leu Leu Gly Ser Met Leu  
 100 105 110  
 acc tgt aaa gct gcc atg agg gct atg att caa caa cag gga ggg tct 561  
 Thr Cys Lys Ala Ala Met Arg Ala Met Ile Gln Gln Gln Gly Gly Ser  
 115 120 125  
 att gtt aat gta gga agc att gtt ggc tta aaa ggc aac tct ggc cag 609  
 Ile Val Asn Val Gly Ser Ile Val Gly Leu Lys Gly Asn Ser Gly Gln  
 130 135 140 145

tcc gtt tac agt gcc agt aaa gga gga tta gtt gga ttt tca cgt gct	657
Ser Val Tyr Ser Ala Ser Lys Gly Gly Leu Val Gly Phe Ser Arg Ala	
150 155 160	
ctt gct aaa gag gta gca aga aag aaa att aga gtg aat gta gtt gca	705
Leu Ala Lys Glu Val Ala Arg Lys Lys Ile Arg Val Asn Val Val Ala	
165 170 175	
cca gga ttt gta cac aca gat atg acg aaa gac ttg aaa gaa gaa cat	753
Pro Gly Phe Val His Thr Asp Met Thr Lys Asp Leu Lys Glu Glu His	
180 185 190	
tta aag aaa aat att cct ctt ggg agg ttt gga gaa act att gag gtg	801
Leu Lys Lys Asn Ile Pro Leu Gly Arg Phe Gly Glu Thr Ile Glu Val	
195 200 205	
gca cat gcg gtt gtg ttt ctt tta gaa tca ccg tat att aca ggg cat	849
Ala His Ala Val Val Phe Leu Leu Glu Ser Pro Tyr Ile Thr Gly His	
210 215 220 225	
gtt ctg gta gtg gat ggg gga tta caa ctc att ttg taatttgcag	895
Val Leu Val Val Asp Gly Gly Leu Gln Leu Ile Leu	
230 235	
attattcagt tataggggtg attagcatca agggcacact ttggctactg attagacaat	955
tatacctaca tgggtaacat gtgctaataca aacctgctga tgctacaaat gttaatttct	1015
gtctttataa aaatatgtct caaaagaa	1043

&lt;210&gt; 14

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Met Asp Lys Val Cys Ala Ile Phe Gly Gly Ser Arg Gly Ile Gly Arg	
1 5 10 15	
Ala Val Ala Gln Leu Met Ala Arg Lys Gly Tyr Arg Leu Ala Ile Ile	
20 25 30	
Ala Arg Asn Leu Glu Gly Ala Lys Ala Ala Ala Gly Asp Leu Gly Gly	
35 40 45	
Asp His Leu Ala Phe Ser Cys Asp Val Ala Lys Glu His Asp Val Gln	
50 55 60	
Asn Thr Phe Glu Glu Met Glu Lys His Leu Gly Arg Val Asn Phe Leu	
65 70 75 80	
Val Asn Ala Ala Gly Ile Asn Arg Asp Ser Leu Leu Val Arg Thr Lys	
85 90 95	
Thr Glu Asp Met Val Ser Gln Leu His Thr Asn Leu Leu Gly Ser Met	
100 105 110	
Leu Thr Cys Lys Ala Ala Met Arg Ala Met Ile Gln Gln Gln Gly Gly	
115 120 125	
Ser Ile Val Asn Val Gly Ser Ile Val Gly Leu Lys Gly Asn Ser Gly	
130 135 140	
Gln Ser Val Tyr Ser Ala Ser Lys Gly Gly Leu Val Gly Phe Ser Arg	
145 150 155 160	
Ala Leu Ala Lys Glu Val Ala Arg Lys Lys Ile Arg Val Asn Val Val	
165 170 175	
Ala Pro Gly Phe Val His Thr Asp Met Thr Lys Asp Leu Lys Glu Glu	

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      180              185              190
His Leu Lys Lys Asn Ile Pro Leu Gly Arg Phe Gly Glu Thr Ile Glu
      195              200              205
Val Ala His Ala Val Val Phe Leu Leu Glu Ser Pro Tyr Ile Thr Gly
      210              215              220
His Val Leu Val Val Asp Gly Gly Leu Gln Leu Ile Leu
      225              230              235

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<210> 15  
 <211> 714  
 <212> DNA  
 <213> Homo sapiens

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<400> 15
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gccgccgccg gtgacctcgg cggagatcat ttggcattta gctgtgatgt tgctaaagaa      180
catgatgttc aaaatacatt tgaagagatg gagaaacatt taggtcgagt aaatttcttg      240
gtaaatgcag ctggtattaa cagggatagt ctttttagtaa gaacaaaaac tgaagatatg      300
gtatctcagc ttcatactaa cctcttgggg tccatgctga cctgtaaagc tgccatgagg      360
gctatgattc aacaacaggg aggggtctatt gttaatgtag gaagcattgt tggcttaaaaa      420
ggcaactctg gccagtcctg ttacagtgcc agtaaaggag gattagttgg attttcacgt      480
gctcttgcta aagaggtagc aagaaagaaa attagagtga atgtagttgc accaggattt      540
gtacacacag atatgacgaa agacttgaaa gaagaacatt taaagaaaaa tattcctctt      600
gggagggttg gagaaactat tgaggtggca catgcggttg tgtttctttt agaatcacccg      660
tatattacag ggcattgtct ggtagtggat gggggattac aactcatttt gtaa      714

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<210> 16  
 <211> 2156  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39)...(1499)

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<400> 16
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                                Met Ala Gly Thr Asn Thr
                                1              5

ctt ttg atg ctg gaa aac ttc ata gat gga aaa ttt tta cct tgt agc      104
Leu Leu Met Leu Glu Asn Phe Ile Asp Gly Lys Phe Leu Pro Cys Ser
      10              15              20

tca tat ata gat tct tac gac cca tca aca ggg gaa gtg tat tgc aga      152
Ser Tyr Ile Asp Ser Tyr Asp Pro Ser Thr Gly Glu Val Tyr Cys Arg
      25              30              35

gtg cca aat agt gga aaa gac gag atc gaa gcc gcg gtc aag gcc gcc      200
Val Pro Asn Ser Gly Lys Asp Glu Ile Glu Ala Ala Val Lys Ala Ala
      40              45              50

aga gaa gcc ttt ccc agc tgg tca tcc cgc agc ccc cag gag cgc tca      248
Arg Glu Ala Phe Pro Ser Trp Ser Ser Arg Ser Pro Gln Glu Arg Ser
      55              60              65              70

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cgg gtc ctg aac cag gtg gcg gat ttg ctg gag cag tcc ctg gag gag Arg Val Leu Asn Gln Val Ala Asp Leu Leu Glu Gln Ser Leu Glu Glu 75 80 85	296
ttt gcc cag gcc gag tct aaa gac caa ggg aaa acc tta gca ctg gca Phe Ala Gln Ala Glu Ser Lys Asp Gln Gly Lys Thr Leu Ala Leu Ala 90 95 100	344
aga acc atg gac att ccc cgg tct gtg cag aac ttc agg ttc ttc gct Arg Thr Met Asp Ile Pro Arg Ser Val Gln Asn Phe Arg Phe Phe Ala 105 110 115	392
tcc tcc agc ctg cac cac acg tca gag tgc acg cag atg gac cac ctg Ser Ser Ser Leu His His Thr Ser Glu Cys Thr Gln Met Asp His Leu 120 125 130	440
ggc tgc atg cac tac acg gtg cgg gcc ccg gtg gga gtc gct ggt ctg Gly Cys Met His Tyr Thr Val Arg Ala Pro Val Gly Val Ala Gly Leu 135 140 145 150	488
atc agc ccc tgg aat ttg cca ctc tac ttg ctg acc tgg aag ata gct Ile Ser Pro Trp Asn Leu Pro Leu Tyr Leu Leu Thr Trp Lys Ile Ala 155 160 165	536
cca gcg atg gct gca ggg aac act gtg ata gcc aag ccc agt gag ctg Pro Ala Met Ala Ala Gly Asn Thr Val Ile Ala Lys Pro Ser Glu Leu 170 175 180	584
act tca gtg act gcg tgg atg ttg tgc aaa ctc ctg gat aaa gca ggt Thr Ser Val Thr Ala Trp Met Leu Cys Lys Leu Leu Asp Lys Ala Gly 185 190 195	632
gtt cca cca ggt gtg gtc aat att gtg ttt gga acc ggg ccc agg gtg Val Pro Pro Gly Val Val Asn Ile Val Phe Gly Thr Gly Pro Arg Val 200 205 210	680
ggt gag gcc ctg gtg tcc cac cca gag gtg ccc ctg atc tcc ttc acc Gly Glu Ala Leu Val Ser His Pro Glu Val Pro Leu Ile Ser Phe Thr 215 220 225 230	728
ggg agc cag ccc acc gct gag cgg atc acc cag ctg agc gct ccc cac Gly Ser Gln Pro Thr Ala Glu Arg Ile Thr Gln Leu Ser Ala Pro His 235 240 245	776
tgc aaa aag ctc tcc ctg gag ctg ggg ggc aag aat cct gcc atc atc Cys Lys Lys Leu Ser Leu Glu Leu Gly Gly Lys Asn Pro Ala Ile Ile 250 255 260	824
ttt gag gac gcc aac ctg gat gag tgc att ccg gca acc gtc agg tcc Phe Glu Asp Ala Asn Leu Asp Glu Cys Ile Pro Ala Thr Val Arg Ser 265 270 275	872
agc ttt gcc aac cag ggt gaa atc tgt ctc tgt acc agc agg atc ttt Ser Phe Ala Asn Gln Gly Glu Ile Cys Leu Cys Thr Ser Arg Ile Phe 280 285 290	920
gtc cag aag agc atc tat agt gaa ttt tta aag aga ttt gta gaa gct	968

Val Gln Lys Ser Ile Tyr Ser Glu Phe Leu Lys Arg Phe Val Glu Ala	
295 300 305 310	
acc aga aag tgg aaa gtc ggc att ccc tct gat cca ctg gtg agc ata	1016
Thr Arg Lys Trp Lys Val Gly Ile Pro Ser Asp Pro Leu Val Ser Ile	
315 320 325	
ggg gct ctg ata agt aaa gca cat ttg gag aaa gtc aga agt tac gtc	1064
Gly Ala Leu Ile Ser Lys Ala His Leu Glu Lys Val Arg Ser Tyr Val	
330 335 340	
aag aga gct ctt gct gaa ggt gcc caa att tgg tgc ggt gag gga gtg	1112
Lys Arg Ala Leu Ala Glu Gly Ala Gln Ile Trp Cys Gly Glu Gly Val	
345 350 355	
gat aag ttg agc ctc cct gcc agg aac cag gca ggc tac ttt atg ctt	1160
Asp Lys Leu Ser Leu Pro Ala Arg Asn Gln Ala Gly Tyr Phe Met Leu	
360 365 370	
ccc acg gtg ata aca gac att aag gat gaa tcc tgc tgc atg acg gaa	1208
Pro Thr Val Ile Thr Asp Ile Lys Asp Glu Ser Cys Cys Met Thr Glu	
375 380 385 390	
gag ata ttt ggt cca gtg acg tgt gtc gtc ccc ttt gat agt gaa gag	1256
Glu Ile Phe Gly Pro Val Thr Cys Val Val Pro Phe Asp Ser Glu Glu	
395 400 405	
gag gtg att gaa aga gcc aac aac gtt aag tat ggg ctg ggg gct acc	1304
Glu Val Ile Glu Arg Ala Asn Asn Val Lys Tyr Gly Leu Gly Ala Thr	
410 415 420	
gtg tgg tcc agc aat gtg ggg cgc gtc cac cgg gtg gct aag aag ctg	1352
Val Trp Ser Ser Asn Val Gly Arg Val His Arg Val Ala Lys Lys Leu	
425 430 435	
cag tct ggc ttg gtc tgg acc aac tgc tgg ctc atc agg gag ctg aac	1400
Gln Ser Gly Leu Val Trp Thr Asn Cys Trp Leu Ile Arg Glu Leu Asn	
440 445 450	
ctt cct ttc ggg ggg atg aag agt tct gga ata ggt aga gag gga gcc	1448
Leu Pro Phe Gly Gly Met Lys Ser Ser Gly Ile Gly Arg Glu Gly Ala	
455 460 465 470	
aag gac tct tac gac ttc ttc act gag atc aaa acc atc acc gtt aaa	1496
Lys Asp Ser Tyr Asp Phe Phe Thr Glu Ile Lys Thr Ile Thr Val Lys	
475 480 485	
cac tgatctttgc taatgggtgga gccactatgg ccaatgcctg gctgcaggca	1549
His	
tcagttgttc aatgtggtag atgaaaatca tggcatgaat tccagctatg ccttgacttg	1609
gcagaagggtt atctctagct tatectcagt tcttagtaac tttaccact agtgaagaga	1669
tactgtctat tttcaatgtg gactcggaaa aaaagactta taagtaggaa gatagaacaa	1729
tgatgccagt tgtcaggctc ctcccagggtt atgttttcat agtgtttctt tcatcatctt	1789
cattgaactc ttgggaatct ccagataatc agattatttc atttggtaaa ttttaaaaaa	1849
tatgcaatca ggcacagtgc ctcatgccta taatcccagc actttgggag gccaaagggtg	1909

1969  
2029  
2089  
2149  
2156

<400>	17															
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1				5					10					15		
Lys	Phe	Leu	Pro	Cys	Ser	Ser	Tyr	Ile	Asp	Ser	Tyr	Asp	Pro	Ser	Thr	
			20					25					30			
Gly	Glu	Val	Tyr	Cys	Arg	Val	Pro	Asn	Ser	Gly	Lys	Asp	Glu	Ile	Glu	
		35					40					45				
Ala	Ala	Val	Lys	Ala	Ala	Arg	Glu	Ala	Phe	Pro	Ser	Trp	Ser	Ser	Arg	
	50					55					60					
Ser	Pro	Gln	Glu	Arg	Ser	Arg	Val	Leu	Asn	Gln	Val	Ala	Asp	Leu	Leu	
65					70					75				80		
Glu	Gln	Ser	Leu	Glu	Phe	Ala	Gln	Ala	Glu	Ser	Lys	Asp	Gln	Gly		
				85				90					95			
Lys	Thr	Leu	Ala	Leu	Ala	Arg	Thr	Met	Asp	Ile	Pro	Arg	Ser	Val	Gln	
			100					105					110			
Asn	Phe	Arg	Phe	Phe	Ala	Ser	Ser	Ser	Leu	His	His	Thr	Ser	Glu	Cys	
		115					120					125				
Thr	Gln	Met	Asp	His	Leu	Gly	Cys	Met	His	Tyr	Thr	Val	Arg	Ala	Pro	
	130					135					140					
Val	Gly	Val	Ala	Gly	Leu	Ile	Ser	Pro	Trp	Asn	Leu	Pro	Leu	Tyr	Leu	
145					150					155					160	
Leu	Thr	Trp	Lys	Ile	Ala	Pro	Ala	Met	Ala	Ala	Gly	Asn	Thr	Val	Ile	
				165					170					175		
Ala	Lys	Pro	Ser	Glu	Leu	Thr	Ser	Val	Thr	Ala	Trp	Met	Leu	Cys	Lys	
		180						185					190			
Leu	Leu	Asp	Lys	Ala	Gly	Val	Pro	Pro	Gly	Val	Val	Asn	Ile	Val	Phe	
		195					200					205				
Gly	Thr	Gly	Pro	Arg	Val	Gly	Glu	Ala	Leu	Val	Ser	His	Pro	Glu	Val	
	210					215					220					
Pro	Leu	Ile	Ser	Phe	Thr	Gly	Ser	Gln	Pro	Thr	Ala	Glu	Arg	Ile	Thr	
225					230					235					240	
Gln	Leu	Ser	Ala	Pro	His	Cys	Lys	Lys	Leu	Ser	Leu	Glu	Leu	Gly	Gly	
				245					250					255		
Lys	Asn	Pro	Ala	Ile	Ile	Phe	Glu	Asp	Ala	Asn	Leu	Asp	Glu	Cys	Ile	
			260					265					270			
Pro	Ala	Thr	Val	Arg	Ser	Ser	Phe	Ala	Asn	Gln	Gly	Glu	Ile	Cys	Leu	
		275					280					285				
Cys	Thr	Ser	Arg	Ile	Phe	Val	Gln	Lys	Ser	Ile	Tyr	Ser	Glu	Phe	Leu	
	290					295					300					
Lys	Arg	Phe	Val	Glu	Ala	Thr	Arg	Lys	Trp	Lys	Val	Gly	Ile	Pro	Ser	
305					310					315					320	
Asp	Pro	Leu	Val	Ser	Ile	Gly	Ala	Leu	Ile	Ser	Lys	Ala	His	Leu	Glu	
				325					330			</				

	355		360		365	
Ala	Gly Tyr Phe Met Leu Pro Thr Val Ile Thr Asp Ile Lys Asp Glu					
	370		375		380	
Ser	Cys Cys Met Thr Glu Ile Phe Gly Pro Val Thr Cys Val Val					
385		390		395		400
Pro	Phe Asp Ser Glu Glu Glu Val Ile Glu Arg Ala Asn Asn Val Lys					
	405		410		415	
Tyr	Gly Leu Gly Ala Thr Val Trp Ser Ser Asn Val Gly Arg Val His					
	420		425		430	
Arg	Val Ala Lys Lys Leu Gln Ser Gly Leu Val Trp Thr Asn Cys Trp					
	435		440		445	
Leu	Ile Arg Glu Leu Asn Leu Pro Phe Gly Gly Met Lys Ser Ser Gly					
	450		455		460	
Ile	Gly Arg Glu Gly Ala Lys Asp Ser Tyr Asp Phe Phe Thr Glu Ile					
465		470		475		480
Lys	Thr Ile Thr Val Lys His					
	485					

&lt;210&gt; 18

&lt;211&gt; 1464

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

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tgtagctcat	atatagattc	ttacgaccca	tcaacagggg	aagtgtattg	cagagtgcc	120
aatagtggaa	aagacgagat	cgaagccg	gtcaagggc	ccagagaagc	cttcccagc	180
tggtcatccc	gcagccccca	ggagcgctca	cgggtcctga	accaggtggc	ggatttgctg	240
gagcagtc	tggaggagtt	tgcccaggcc	gagtctaaag	accaagggaa	aaccttagca	300
ctggcaagaa	ccatggacat	tccccggctc	gtgcagaact	tcaggttctt	cgttctctcc	360
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gtgcggggccc	cggtgaggag	cgctggctc	atcagcccct	ggaatttgcc	actctacttg	480
ctgacctgga	agatagctcc	agcgatggct	gcagggaa	ctgtgatagc	caagcccagt	540
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cacccagagg	tgcccctgat	ctccttcacc	gggagccagc	ccaccgctga	gcggatcacc	720
cagctgagcg	ctccccactg	caaaaagctc	tccctggagc	tggggggcaa	gaatcctgcc	780
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gatccactgg	tgagcatagg	tgctctgata	agtaaagcac	atttggagaa	agtcagaagt	1020
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ccctttgata	gtgaagagga	ggtgattgaa	agagccaaca	acgttaagta	tgggctgggg	1260
gctaccgtgt	ggtccagcaa	tgtggggcgc	gtccaccggg	tggctaagaa	gctgcagtct	1320
ggcttggtct	ggaccaactg	ctggctcatc	agggagctga	accttctctt	cgggggggatg	1380
aagagttctg	gaataggtag	agaggggagc	aaggactctt	acgacttctt	cactgagatc	1440
aaaaccatca	ccgttaaaca	ctga				1464

&lt;210&gt; 19

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence



&lt;400&gt; 19

```

Lys Val Ala Leu Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Ala Ile
 1           5           10           15
Ala Lys Arg Leu Ala Lys Glu Gly Ala Lys Val Val Val Ala Asp Arg
 20           25           30
Asn Glu Glu Lys Leu Glu Lys Gly Ala Val Ala Lys Glu Leu Lys Glu
 35           40           45
Leu Gly Gly Asn Asp Lys Asp Arg Ala Leu Ala Ile Gln Leu Asp Val
 50           55           60
Thr Asp Glu Glu Ser Val Ala Ala Val Glu Gln Ala Val Glu Arg Leu
 65           70           75           80
Gly Arg Leu Asp Val Leu Val Asn Asn Ala Gly Gly Ile Ile Leu Leu
 85           90           95
Arg Pro Gly Pro Phe Ala Glu Leu Ser Arg Thr Met Glu Glu Asp Trp
100          105          110
Asp Arg Val Ile Asp Val Asn Leu Thr Gly Val Phe Leu Leu Thr Arg
115          120          125
Ala Val Leu Pro Leu Met Ala Met Lys Lys Arg Gly Gly Gly Arg Ile
130          135          140
Val Asn Ile Ser Ser Val Ala Gly Arg Lys Glu Gly Gly Leu Val Gly
145          150          155          160
Val Pro Gly Gly Ser Ala Tyr Ser Ala Ser Lys Ala Ala Val Ile Gly
165          170          175
Leu Thr Arg Ser Leu Ala Leu Glu Leu Ala Pro His Gly Ile Arg Val
180          185          190
Asn Ala Val Ala Pro Gly Gly Val Asp Thr Asp
195          200

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&lt;210&gt; 20

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 20

```

Gly Arg Leu Gly Glu Pro Glu Glu Ile Ala Asn Ala Val Val Phe Leu
 1           5           10           15
Ala Ser Asp Ala Ala Ser Tyr Ile Thr Gly Gln Thr Leu Val Val
 20           25           30

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&lt;210&gt; 21

&lt;211&gt; 493

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 21

```

Glu Trp Val Asp Ser Ala Ser Gly Lys Thr Phe Glu Val Val Asn Pro
 1           5           10           15
Ala Asn Lys Gly Glu Val Ile Gly Arg Val Pro Glu Ala Thr Ala Glu
 20           25           30
Asp Val Asp Ala Ala Val Lys Ala Ala Lys Glu Ala Phe Lys Ser Gly

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35					40					45					
Pro	Trp	Trp	Ala	Lys	Val	Pro	Ala	Ser	Glu	Arg	Ala	Arg	Ile	Leu	Arg
50						55					60				
Lys	Leu	Ala	Asp	Leu	Ile	Glu	Glu	Arg	Glu	Asp	Glu	Leu	Ala	Ala	Leu
65					70					75					80
Glu	Thr	Leu	Asp	Leu	Gly	Lys	Pro	Leu	Ala	Glu	Ala	Lys	Gly	Asp	Thr
				85					90					95	
Glu	Val	Gly	Arg	Ala	Ile	Asp	Glu	Ile	Arg	Tyr	Tyr	Ala	Gly	Trp	Ala
			100					105					110		
Arg	Lys	Leu	Met	Gly	Glu	Arg	Arg	Val	Ile	Pro	Ser	Leu	Ala	Thr	Asp
		115					120					125			
Gly	Asp	Glu	Glu	Leu	Asn	Tyr	Thr	Arg	Arg	Glu	Pro	Leu	Gly	Val	Val
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Leu	Ala	Pro	Ala	Leu	Ala	Ala	Gly	Asn	Thr	Val	Val	Leu	Lys	Pro	Ser
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Glu	Gln	Thr	Pro	Leu	Thr	Ala	Leu	Leu	Leu	Ala	Glu	Leu	Ile	Glu	Glu
			180				185						190		
Ala	Gly	Ala	Asn	Asn	Leu	Pro	Lys	Gly	Val	Val	Asn	Val	Val	Pro	Gly
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Phe	Gly	Ala	Glu	Val	Gly	Gln	Ala	Leu	Leu	Ser	His	Pro	Asp	Ile	Asp
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Lys	Ile	Ser	Phe	Thr	Gly	Ser	Thr	Glu	Val	Gly	Lys	Leu	Ile	Met	Glu
225				230						235					240
Ala	Ala	Ala	Ala	Lys	Asn	Leu	Lys	Lys	Val	Thr	Leu	Glu	Leu	Gly	Gly
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Lys	Ser	Pro	Val	Ile	Val	Phe	Asp	Asp	Ala	Asp	Leu	Asp	Lys	Ala	Val
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Glu	Arg	Ile	Val	Phe	Gly	Ala	Phe	Gly	Asn	Ala	Gly	Gln	Val	Cys	Ile
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Ala	Pro	Ser	Arg	Leu	Leu	Val	His	Glu	Ser	Ile	Tyr	Asp	Glu	Phe	Val
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Glu	Lys	Leu	Lys	Glu	Arg	Val	Lys	Lys	Leu	Lys	Leu	Ile	Gly	Asp	Pro
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Leu	Asp	Ser	Asp	Thr	Asn	Ile	Tyr	Gly	Pro	Leu	Ile	Ser	Glu	Gln	Gln
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Phe	Asp	Arg	Val	Leu	Trp	Ser	Tyr	Ile	Glu	Asp	Gly	Lys	Glu	Glu	Gly
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Ala	Lys	Val	Leu	Cys	Gly	Gly	Glu	Arg	Asp	Glu	Ser	Lys	Glu	Tyr	Leu
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Gly	Gly	Gly	Tyr	Tyr	Val	Gln	Pro	Thr	Ile	Phe	Thr	Asp	Val	Thr	Pro
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Asp	Met	Lys	Ile	Met	Lys	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Pro	Ile
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Ile	Lys	Phe	Lys	Asp	Leu	Asp	Glu	Ala	Ile	Glu	Leu	Ala	Asn	Asp	Thr
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Glu	Tyr	Gly	Leu	Ala	Ala	Tyr	Val	Phe	Thr	Lys	Asp	Ile	Leu	Ala	Arg
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Ala	Phe	Arg	Val	Ala	Lys	Ala	Leu	Glu	Ala	Gly	Ile	Val	Trp	Val	Asn
	435						440					445			
Asp	Val	Cys	Val	His	Ala	Ala	Glu	Pro	Gln	Leu	Pro	Phe	Gly	Gly	Val
	450				455					460					
Lys	Gln	Ser	Ser	Gly	Ile	Gly	Arg	Glu	His	Gly	Gly	Lys	Tyr	Gly	Leu
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 ccctactcca gagcagagaa tgcagtggaa cccaggctcc tgatatccat ctgggtgagc 180  
 cagccagagg gaccggctgt gtcagaggca agcaaacaag tattagagtg caagactgtg 240  
 ggcgagagaga ggaagcccgga gccgccagca gggagcttcg gagagagaaa gccaggaac 300  
 atcccagaga gagctgggcc catcctcagc cctacccagc cccgcagccc ctagccctcc 360  
 gccagaaaac ccagccctgt ccggcggtgcc gctcttctcc tccaggccgg ctgctgctgc 420  
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 Met Ala Val Tyr Arg Leu  
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tgt gtg acc act ggt ccc tac ctg agg gcc ggc aca ctg gac aac atc 524  
 Cys Val Thr Thr Gly Pro Tyr Leu Arg Ala Gly Thr Leu Asp Asn Ile  
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 Ser Val Thr Leu Val Gly Thr Cys Gly Glu Ser Pro Lys Gln Arg Leu  
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gat cga atg ggc agg gac ttc gcc cct gga tcg gta cag aag tac aag 620  
 Asp Arg Met Gly Arg Asp Phe Ala Pro Gly Ser Val Gln Lys Tyr Lys  
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gtg cgt tgc aca gcg gag ctg ggt gag ctc ttg ctg ctg cgt gta cac 668  
 Val Arg Cys Thr Ala Glu Leu Gly Glu Leu Leu Leu Leu Arg Val His  
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aag gag cgc tac gct ttc ttc cgc aag gac tct tgg tac tgt agc cgc 716  
 Lys Glu Arg Tyr Ala Phe Phe Arg Lys Asp Ser Trp Tyr Cys Ser Arg  
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atc tgt gtc acc gaa ccg gat ggt agt gta tcc cac ttc ccc tgc tat 764  
 Ile Cys Val Thr Glu Pro Asp Gly Ser Val Ser His Phe Pro Cys Tyr  
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cag tgg att gaa ggc tac tgc acc gtg gag ctg agg cca gga aca gca 812  
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aga act att tgt cag gac tct ctt ccc ctc ctc ctg gat cac agg aca 860  
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Pro Gly Phe Pro Cys Met Val Asp Val Asn Ser Phe Gln Glu Met Glu	
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Ser Asp Lys Lys Phe Ala Leu Thr Lys Thr Thr Thr Cys Val Asp Gln	
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Gly Asp Ser Ser Gly Asn Arg Tyr Leu Pro Gly Phe Pro Met Lys Ile	
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Asp Ile Pro Ser Leu Met Tyr Met Glu Pro Asn Val Arg Tyr Ser Ala	
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acc aag acg atc tcg ctg ctc ttc aat gcc atc cct gcg tcc ttg gga	1148
Thr Lys Thr Ile Ser Leu Leu Phe Asn Ala Ile Pro Ala Ser Leu Gly	
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Met Lys Leu Arg Gly Leu Leu Asp Arg Lys Gly Ser Trp Lys Lys Leu	
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gat gac atg cag aac atc ttc tgg tgc cat aag acc ttc acg aca aag	1244
Asp Asp Met Gln Asn Ile Phe Trp Cys His Lys Thr Phe Thr Thr Lys	
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tat gtc aca gag cac tgg tgt gaa gat cac ttc ttt ggg tac cag tac	1292
Tyr Val Thr Glu His Trp Cys Glu Asp His Phe Phe Gly Tyr Gln Tyr	
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Leu Asn Gly Val Asn Pro Val Met Leu His Cys Ile Ser Ser Leu Pro	
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Ser Lys Leu Pro Val Thr Asn Asp Met Val Ala Pro Leu Leu Gly Gln	
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gac aca tgc ctg cag aca gag cta gag agg ggg aac atc ttc cta gcg	1436
Asp Thr Cys Leu Gln Thr Glu Leu Glu Arg Gly Asn Ile Phe Leu Ala	
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gac tac tgg atc ctg gcg gag gcc ccc acc cac tgc cta aac ggc cgc	1484
Asp Tyr Trp Ile Leu Ala Glu Ala Pro Thr His Cys Leu Asn Gly Arg	
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Gln Gln Tyr Val Ala Ala Pro Leu Cys Leu Leu Trp Leu Ser Pro Gln	
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Gly Ala Leu Val Pro Leu Ala Ile Gln Leu Ser Gln Thr Pro Gly Pro	
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ccc cac act cga tac acg ctg cag gtg aac acc atc gcg agg gcc acg Pro His Thr Arg Tyr Thr Leu Gln Val Asn Thr Ile Ala Arg Ala Thr 440 445 450	1820
ctg ctc aac ccc gag ggc ctc gtg gac cag gtc acg tcc atc ggg agg Leu Leu Asn Pro Glu Gly Leu Val Asp Gln Val Thr Ser Ile Gly Arg 455 460 465 470	1868
caa ggc ctc atc tac ctc atg agc acg ggc ctg gcc cac ttc acc tac Gln Gly Leu Ile Tyr Leu Met Ser Thr Gly Leu Ala His Phe Thr Tyr 475 480 485	1916
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Gly Ala Trp Met Pro Asn Ala Pro Ser Ser Met Arg Gln Pro Pro Pro  
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cag acc aag ggg acc acc acc ctg aag act tac cta gac acc ctc cct 2348  
 Gln Thr Lys Gly Thr Thr Leu Lys Thr Tyr Leu Asp Thr Leu Pro  
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gaa gtg aac atc agc tgt aac aac ctc ctc ctc ttc tgg ttg gtt agc 2396  
 Glu Val Asn Ile Ser Cys Asn Asn Leu Leu Leu Phe Trp Leu Val Ser  
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caa gaa ccc aag gac cag agg ccc ctg ggc acc tac cca gat gag cac 2444  
 Gln Glu Pro Lys Asp Gln Arg Pro Leu Gly Thr Tyr Pro Asp Glu His  
 650 655 660

ttc aca gag gag gcc ccg agg cgg agc atc gcc gcc ttc cag agc cgc 2492  
 Phe Thr Glu Glu Ala Pro Arg Arg Ser Ile Ala Ala Phe Gln Ser Arg  
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 680 685 690

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 Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu Asn Ser Val Ser  
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 35 40 45  
 Ser Val Gln Lys Tyr Lys Val Arg Cys Thr Ala Glu Leu Gly Glu Leu  
 50 55 60

Leu Leu Leu Arg Val His Lys Glu Arg Tyr Ala Phe Phe Arg Lys Asp  
 65 70 75 80  
 Ser Trp Tyr Cys Ser Arg Ile Cys Val Thr Glu Pro Asp Gly Ser Val  
 85 90 95  
 Ser His Phe Pro Cys Tyr Gln Trp Ile Glu Gly Tyr Cys Thr Val Glu  
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 Leu Arg Pro Gly Thr Ala Arg Thr Ile Cys Gln Asp Ser Leu Pro Leu  
 115 120 125  
 Leu Leu Asp His Arg Thr Arg Glu Leu Arg Ala Arg Gln Glu Cys Tyr  
 130 135 140  
 Arg Trp Lys Ile Tyr Ala Pro Gly Phe Pro Cys Met Val Asp Val Asn  
 145 150 155 160  
 Ser Phe Gln Glu Met Glu Ser Asp Lys Lys Phe Ala Leu Thr Lys Thr  
 165 170 175  
 Thr Thr Cys Val Asp Gln Gly Asp Ser Ser Gly Asn Arg Tyr Leu Pro  
 180 185 190  
 Gly Phe Pro Met Lys Ile Asp Ile Pro Ser Leu Met Tyr Met Glu Pro  
 195 200 205  
 Asn Val Arg Tyr Ser Ala Thr Lys Thr Ile Ser Leu Leu Phe Asn Ala  
 210 215 220  
 Ile Pro Ala Ser Leu Gly Met Lys Leu Arg Gly Leu Leu Asp Arg Lys  
 225 230 235 240  
 Gly Ser Trp Lys Lys Leu Asp Asp Met Gln Asn Ile Phe Trp Cys His  
 245 250 255  
 Lys Thr Phe Thr Lys Tyr Val Thr Glu His Trp Cys Glu Asp His  
 260 265 270  
 Phe Phe Gly Tyr Gln Tyr Leu Asn Gly Val Asn Pro Val Met Leu His  
 275 280 285  
 Cys Ile Ser Ser Leu Pro Ser Lys Leu Pro Val Thr Asn Asp Met Val  
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 Ala Pro Leu Leu Gly Gln Asp Thr Cys Leu Gln Thr Glu Leu Glu Arg  
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 Gly Asn Ile Phe Leu Ala Asp Tyr Trp Ile Leu Ala Glu Ala Pro Thr  
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 His Cys Leu Asn Gly Arg Gln Gln Tyr Val Ala Ala Pro Leu Cys Leu  
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 Ser Gln Thr Pro Gly Pro Asp Ser Pro Ile Phe Leu Pro Thr Asp Ser  
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 Glu Trp Asp Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ser Glu Phe  
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 Ile Tyr Lys Leu Leu Leu Pro His Thr Arg Tyr Thr Leu Gln Val Asn  
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 Thr Ile Ala Arg Ala Thr Leu Leu Asn Pro Glu Gly Leu Val Asp Gln  
 450 455 460  
 Val Thr Ser Ile Gly Arg Gln Gly Leu Ile Tyr Leu Met Ser Thr Gly  
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 485 490 495  
 Ala Arg Gly Val Leu Ala Ile Pro Asn Tyr His Tyr Arg Asp Asp Gly  
 500 505 510  
 Leu Lys Ile Trp Ala Ala Ile Glu Ser Phe Val Ser Glu Ile Val Gly

515	520	525
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Ala Trp Thr Gly Glu Ile Phe Ala Gln Ala Phe Leu Gly Arg Glu Ser		
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Ser Gly Phe Pro Ser Arg Leu Cys Thr Pro Gly Glu Met Val Lys Phe		
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Leu Thr Ala Ile Ile Phe Asn Cys Ser Ala Gln His Ala Ala Val Asn		
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Ser Gly Gln His Asp Phe Gly Ala Trp Met Pro Asn Ala Pro Ser Ser		
595	600	605
Met Arg Gln Pro Pro Pro Gln Thr Lys Gly Thr Thr Thr Leu Lys Thr		
610	615	620
Tyr Leu Asp Thr Leu Pro Glu Val Asn Ile Ser Cys Asn Asn Leu Leu		
625	630	635
Leu Phe Trp Leu Val Ser Gln Glu Pro Lys Asp Gln Arg Pro Leu Gly		
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Thr Tyr Pro Asp Glu His Phe Thr Glu Glu Ala Pro Arg Arg Ser Ile		
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Ala Ala Phe Gln Ser Arg Leu Ala Gln Ile Ser Arg Asp Ile Gln Glu		
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Arg Asn Gln Gly Leu Ala Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu		
690	695	700
Ile Glu Asn Ser Val Ser Ile		
705	710	

&lt;210&gt; 24

&lt;211&gt; 2136

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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&lt;210&gt; 25

&lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 25

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Leu	Asp	Pro	Ala	Val	Tyr	Gly	Asp	Gln	Thr	Ser	Thr	Ile	Thr	Lys	Glu
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His	Leu	Glu	Leu	Asn	Leu	Gly	Gly	Leu	Thr	Val	Glu	Glu	Ala	Leu	Gln
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Leu	Asn	Lys	Ile	Asn	Ser	Leu	Thr	Ser	Thr	Lys	Leu	Tyr	Ala	Thr	Arg
			85						90					95	
Thr	Leu	Leu	Phe	Leu	Lys	Asp	Asp	Gly	Thr	Leu	Lys	Pro	Leu	Ala	Ile
			100					105					110		
Glu	Leu	Ser	Leu	Pro	His	Pro	Asp	Gly	Asp	Pro	Phe	Gly	Ala	Val	Ser
		115					120					125			
Lys	Val	Phe	Leu	Pro	Ala	Asp	Glu	Gly	Val	Glu	Ser	Ser	Ile	Trp	Leu
	130					135					140				
Leu	Ala	Lys	Ala	Tyr	Val	Arg	Val	Asn	Asp	Ser	Gly	Tyr	His	Gln	Leu
145					150				155					160	
Ile	Ser	His	Trp	Leu	Asn	Thr	His	Ala	Val	Val	Glu	Pro	Phe	Val	Ile
			165					170						175	
Ala	Thr	Asn	Arg	Gln	Leu	Ser	Val	Leu	His	Pro	Ile	Tyr	Lys	Leu	Leu
		180						185					190		
Leu	Pro	His	Tyr	Arg	Asp	Thr	Met	Asn	Ile	Asn	Ala	Leu	Ala	Arg	Gln
		195					200					205			
Ser	Leu	Ile	Asn	Ala	Gly	Gly	Ile	Ile	Glu	Lys	Thr	Phe	Leu	Pro	Gly
	210					215					220				
Lys	Tyr	Gly	Ala	Val	Glu	Met	Ser	Ser	Ala	Val	Tyr	Lys	Lys	Asp	Trp
225					230					235				240	
Val	Phe	Thr	Asp	Gln	Ala	Leu	Pro	Ala	Asp	Leu	Val	Lys	Arg	Gly	Leu
			245						250					255	
Ala	Val	Glu	Asp	Pro	Ser	Ser	Pro	His	Gly	Val	Arg	Leu	Leu	Ile	Glu
		260						265					270		
Asp	Tyr	Pro	Tyr	Ala	Val	Asp	Gly	Leu	Glu	Ile	Trp	Asp	Ala	Ile	Lys
		275					280						285		

```

Thr Trp Val Gln Glu Tyr Val Ser Leu Tyr Tyr Lys Ser Asp Glu Ala
 290                295                300
Val Lys Lys Asp Pro Glu Leu Gln Ala Trp Trp Lys Glu Val Arg Glu
305                310                315                320
Val Gly His Gly Asp Lys Lys Asp Glu Pro Trp Trp Pro Lys Leu Gln
                325                330                335
Thr Arg Glu Asp Leu Ile Glu Val Cys Thr Ile Ile Ile Trp Ile Ala
                340                345                350
Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro Tyr Gly Gly
                355                360                365
Tyr Ile Pro Asn Arg Pro Thr Thr Ser Arg Arg Pro Met Pro Glu Glu
                370                375                380
Gly Pro Val Asp Thr Ala Glu Tyr Glu Glu Leu Ala Lys Asn Pro Glu
385                390                395                400
Lys Ala Leu Leu Lys Thr Ile Thr Ser Gln Leu Gln Ala Leu Leu Asp
                405                410                415
Leu Ser Val Ile Glu Ile Leu Ser Arg His Ala Ser Asp Glu Val Tyr
                420                425                430
Leu Gly Gln Arg Asp Glu Pro Glu Trp Thr Ser Asp Lys Lys Ala Leu
                435                440                445
Glu Ala Phe Lys Arg Phe Gly Lys Lys Leu Ala Glu Ile Glu Lys Lys
                450                455                460
Ile Thr Glu Arg Asn Lys Asp Glu Ser Leu Lys Asn Arg Val Gly Pro
465                470                475                480
Val Lys Leu Pro Tyr Thr Leu Leu Lys Pro Ser
                485                490

```

&lt;210&gt; 26

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 26

```

Val Ser Tyr Gln Leu Ile Val Ala Thr Gly Asp Asp Ser Thr Phe Ala
 1                5                10                15
Gly Thr Thr Gly Lys Val Gly Ile Ser Leu Tyr Gly Glu Lys Gly Glu
                20                25                30
Ser Lys Lys Ile Lys Leu Leu Lys Gly Glu Leu Lys Asn Leu Pro Thr
                35                40                45
Leu Gly Phe Gly Pro Gly Ser Thr Phe Ser Phe Glu Phe Asp Val Asp
                50                55                60
Glu Asp Phe Gly Glu Leu Gly Ala Val Lys Ile Lys Asn Glu His His
65                70                75                80
Ser Leu Asn Ser Asn Pro Thr Asp Asp Glu Trp Phe Leu Lys Ser Ile
                85                90                95
Thr Val Glu Asp Pro Gly Thr Gln Gly Glu Val His Phe Pro Cys Asn
                100                105                110
Ser Trp Val Tyr Gly Lys Thr Pro Lys Glu Tyr Leu Ser Leu Arg Ile
                115                120                125
Cys

```

&lt;210&gt; 27

&lt;211&gt; 157

&lt;212&gt; PRT

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 27

Ala Lys Tyr Lys Val Thr Val Thr Leu Gly Lys Lys Asn Val Leu Asp  
 1 5 10 15  
 Phe Ala Gly Thr Thr Ala Leu Gly Ser Leu Leu Asp Gly Leu Thr Asp  
 20 25 30  
 Leu Leu Gly Arg Gln Ser Val Ser Leu Ser Leu Ile Gly Ala Glu Gly  
 35 40 45  
 Asp Asp Asn Thr Gly Arg Gly Lys Glu Ser Lys Leu Ala Tyr Leu Glu  
 50 55 60  
 Arg Pro Leu Thr Thr Leu Pro Ser Leu Phe Ala Arg Gly Ser Thr Tyr  
 65 70 75 80  
 Glu Phe Glu Phe Asp Val Asp Glu Asp Phe Gly Glu Leu Gly Ala Val  
 85 90 95  
 Lys Ile Lys Asn Glu His Tyr Gly Leu Phe Trp Ser Ser Pro Arg His  
 100 105 110  
 Ser Glu Phe Phe Leu Lys Ser Ile Thr Leu Lys Asp Leu Gly Pro Thr  
 115 120 125  
 Gly Gly Lys Val His Phe Pro Cys Asn Ser Trp Val Tyr Pro Lys Lys  
 130 135 140  
 Lys Pro Gly Tyr Lys Gly Lys Arg Ile Phe Phe Ala Asn  
 145 150 155

&lt;210&gt; 28

&lt;211&gt; 1639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (191)...(1099)

&lt;400&gt; 28

acggactggg cctggcctgg ggcgtccccg cgaagcctgg gcctgtcagg cggttccgtc 60  
 cgggtctcgg ccaccgtcga gttccgtcga gttccgtccc ggccctgctc acagcagcgc 120  
 cctcggagcg cccagcacct ggcggccggcc aggcagcgcg atcctgcggc gtctggccat 180  
 cccgaatgct atg gcc gcc gtc gcc gtc ttg cgg gcc ttc ggg gca agt 229  
 Met Ala Ala Val Ala Val Leu Arg Ala Phe Gly Ala Ser  
 1 5 10  
 ggg ccc atg tgt ctc cgg cgc ggc ccc tgg gcc cag ctc ccc gcc cgc 277  
 Gly Pro Met Cys Leu Arg Arg Gly Pro Trp Ala Gln Leu Pro Ala Arg  
 15 20 25  
 ttc tgc agc cgg gac ccg gcc ggg gcg ggg cgg cgg gag tcg gag ccg 325  
 Phe Cys Ser Arg Asp Pro Ala Gly Ala Gly Arg Arg Glu Ser Glu Pro  
 30 35 40 45  
 cgg ccc acc agc gcg cgg cag ctg gac ggc ata agg aac atc gtc ttg 373  
 Arg Pro Thr Ser Ala Arg Gln Leu Asp Gly Ile Arg Asn Ile Val Leu  
 50 55 60  
 agc aat ccc aag aag agg aac acg ttg tca ctt gca atg ctg aaa tct 421

Ser	Asn	Pro	Lys	Lys	Arg	Asn	Thr	Leu	Ser	Leu	Ala	Met	Leu	Lys	Ser		
			65					70					75				
ctc	caa	agt	gac	att	ctt	cat	gac	gct	gac	agc	aac	gat	ctg	aaa	gtc		469
Leu	Gln	Ser	Asp	Ile	Leu	His	Asp	Ala	Asp	Ser	Asn	Asp	Leu	Lys	Val		
			80					85				90					
att	atc	atc	tcg	gct	gag	ggg	cct	gtg	ttt	tct	tct	ggg	cat	gac	tta		517
Ile	Ile	Ile	Ser	Ala	Glu	Gly	Pro	Val	Phe	Ser	Ser	Gly	His	Asp	Leu		
			95					100				105					
aag	gag	ctg	aca	gag	gag	caa	ggc	cgt	gat	tac	cat	gcc	gaa	gta	ttt		565
Lys	Glu	Leu	Thr	Glu	Glu	Gln	Gly	Arg	Asp	Tyr	His	Ala	Glu	Val	Phe		
110						115				120					125		
cag	acc	tgt	tcc	aag	gtc	atg	atg	cac	atc	cgg	aac	cac	ccc	gtc	ccc		613
Gln	Thr	Cys	Ser	Lys	Val	Met	Met	His	Ile	Arg	Asn	His	Pro	Val	Pro		
				130						135				140			
gtc	att	gcc	atg	gtc	aat	ggc	ctg	gcc	acg	gct	gcc	ggc	tgt	caa	ctg		661
Val	Ile	Ala	Met	Val	Asn	Gly	Leu	Ala	Thr	Ala	Ala	Gly	Cys	Gln	Leu		
			145					150					155				
gtt	gcc	agc	tgc	aac	att	gcc	gtg	gcg	agc	gac	aag	tcc	tct	ttt	gcc		709
Val	Ala	Ser	Cys	Asn	Ile	Ala	Val	Ala	Ser	Asp	Lys	Ser	Ser	Phe	Ala		
			160					165				170					
act	cct	ggg	gtg	aac	gtc	ggg	ctc	ttc	tgt	tct	acc	cct	ggg	gtt	gcc		757
Thr	Pro	Gly	Val	Asn	Val	Gly	Leu	Phe	Cys	Ser	Thr	Pro	Gly	Val	Ala		
			175					180				185					
ttg	gca	aga	gca	gtg	cct	aga	aag	gtg	gcc	ttg	gag	atg	ctc	ttt	act		805
Leu	Ala	Arg	Ala	Val	Pro	Arg	Lys	Val	Ala	Leu	Glu	Met	Leu	Phe	Thr		
190							195			200					205		
ggg	gag	ccc	att	tct	gcc	cag	gag	gcc	ctg	ctc	cac	ggg	ctg	ctt	agc		853
Gly	Glu	Pro	Ile	Ser	Ala	Gln	Glu	Ala	Leu	Leu	His	Gly	Leu	Leu	Ser		
				210					215					220			
aag	gtg	gtg	cca	gag	gcg	gag	ctg	cag	gag	gag	acc	atg	cgg	atc	gct		901
Lys	Val	Val	Pro	Glu	Ala	Glu	Leu	Gln	Glu	Glu	Thr	Met	Arg	Ile	Ala		
			225					230					235				
agg	aag	atc	gcg	tca	ctg	agc	cgt	ccg	gtg	gtg	tcc	ctg	ggc	aaa	gcc		949
Arg	Lys	Ile	Ala	Ser	Leu	Ser	Arg	Pro	Val	Val	Ser	Leu	Gly	Lys	Ala		
			240					245				250					
acc	ttc	tac	aag	cag	ctg	ccc	cag	gac	ctg	ggg	acg	gct	tac	tac	ctc		997
Thr	Phe	Tyr	Lys	Gln	Leu	Pro	Gln	Asp	Leu	Gly	Thr	Ala	Tyr	Tyr	Leu		
			255				260				265						
acc	tcc	cag	gcc	atg	gtg	gac	aac	ctg	gcc	ctg	cgg	gac	ggg	cag	gag		1045
Thr	Ser	Gln	Ala	Met	Val	Asp	Asn	Leu	Ala	Leu	Arg	Asp	Gly	Gln	Glu		
270						275				280					285		
ggc	atc	acg	gcc	ttc	ctc	cag	aag	aga	aaa	cct	gtc	tgg	tca	cac	gag		1093
Gly	Ile	Thr	Ala	Phe	Leu	Gln	Lys	Arg	Lys	Pro	Val	Trp	Ser	His	Glu		

290

295

300

cca gtg tgagtggagg cagaggagtg agggccacgg gcagcgccca ggagcccacc 1149  
Pro Val

ttcccctctg gccagccac cactgcctct cagcttcaac aggtgacagg ctgctttcgt 1209  
gacttgatat tgggtgcata gcatttggcc tacattaaaa gccacaattt catggggaaa 1269  
ggacaaaatg gagagtgact gaggtgctga cctcagtga aggtctggtga accctgcagc 1329  
gggccagcta tgggtgggaag cctggcattt ggggtgctcc ttgcaacgtc ttaagcaagc 1389  
gacccccctg acatagcaaa aggtggcaac ccatggaggc agaaagaagg acgccagcct 1449  
gacccttatc tgaaacgtcc taagcagagt taatcctggc tgctcaggag aggcgacaca 1509  
tttcaaatct ccacgagata ttctccacac agaaaatctt cttgattcta tagagactta 1569  
atcatgccta tggctttgaa taatcttatg tgattttaat aaattaaatc tttatagaga 1629  
aaaaaaaaa 1639

&lt;210&gt; 29

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

Met Ala Ala Val Ala Val Leu Arg Ala Phe Gly Ala Ser Gly Pro Met  
1 5 10 15  
Cys Leu Arg Arg Gly Pro Trp Ala Gln Leu Pro Ala Arg Phe Cys Ser  
20 25 30  
Arg Asp Pro Ala Gly Ala Gly Arg Arg Glu Ser Glu Pro Arg Pro Thr  
35 40 45  
Ser Ala Arg Gln Leu Asp Gly Ile Arg Asn Ile Val Leu Ser Asn Pro  
50 55 60  
Lys Lys Arg Asn Thr Leu Ser Leu Ala Met Leu Lys Ser Leu Gln Ser  
65 70 75 80  
Asp Ile Leu His Asp Ala Asp Ser Asn Asp Leu Lys Val Ile Ile Ile  
85 90 95  
Ser Ala Glu Gly Pro Val Phe Ser Ser Gly His Asp Leu Lys Glu Leu  
100 105 110  
Thr Glu Glu Gln Gly Arg Asp Tyr His Ala Glu Val Phe Gln Thr Cys  
115 120 125  
Ser Lys Val Met Met His Ile Arg Asn His Pro Val Pro Val Ile Ala  
130 135 140  
Met Val Asn Gly Leu Ala Thr Ala Ala Gly Cys Gln Leu Val Ala Ser  
145 150 155 160  
Cys Asn Ile Ala Val Ala Ser Asp Lys Ser Ser Phe Ala Thr Pro Gly  
165 170 175  
Val Asn Val Gly Leu Phe Cys Ser Thr Pro Gly Val Ala Leu Ala Arg  
180 185 190  
Ala Val Pro Arg Lys Val Ala Leu Glu Met Leu Phe Thr Gly Glu Pro  
195 200 205  
Ile Ser Ala Gln Glu Ala Leu Leu His Gly Leu Leu Ser Lys Val Val  
210 215 220  
Pro Glu Ala Glu Leu Gln Glu Thr Met Arg Ile Ala Arg Lys Ile  
225 230 235 240  
Ala Ser Leu Ser Arg Pro Val Val Ser Leu Gly Lys Ala Thr Phe Tyr  
245 250 255  
Lys Gln Leu Pro Gln Asp Leu Gly Thr Ala Tyr Tyr Leu Thr Ser Gln  
260 265 270  
Ala Met Val Asp Asn Leu Ala Leu Arg Asp Gly Gln Glu Gly Ile Thr  
275 280 285

Ala Phe Leu Gln Lys Arg Lys Pro Val Trp Ser His Glu Pro Val  
 290 295 300

<210> 30  
 <211> 912  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
 atggccgcccgc tcgcccgtctt gcgggccttc ggggcaagtg ggcccatgtg tctccggcgc 60  
 ggcccctggg cccagctccc cgcccgttc tgcagccggg acccggccgg ggcggggcgg 120  
 cgggagtcgg agccgcggcc caccagcgcg cggcagctgg acggcataag gaacatcgtc 180  
 ttgagcaatc ccaagaagag gaacacgttg tcaattgcaa tgctgaaatc tctccaaagt 240  
 gacattcttc atgacgctga cagcaacgat ctgaaagtca ttatcatctc ggctgagggg 300  
 cctgtgtttt cttctgggca tgacttaaag gagctgacag aggagcaagg ccgtgattac 360  
 catgccgaag tatttcagac ctggtccaag gtcgatgatc acatccggaa ccaccccgtc 420  
 cccgtcattg ccatgggtcaa tggcctggcc acggctgccc gctgtcaact gggtgccagc 480  
 tgcaacattg ccgtggcgag cgacaagtcc tcttttgcca ctctctgggt gaacgtcggg 540  
 ctcttctgtt ctaccctggg gggtgccttg gcaagagcag tgcctagaaa ggtggccttg 600  
 gagatgctct ttactggtga gcccatcttct gcccaggagg ccctgctcca cgggctgctt 660  
 agcaaggtgg tgccagaggc ggagctgcag gaggagacca tgcggatcgc taggaagatc 720  
 gcgtcactga gccgtccggt ggtgtccctg ggcaaagcca ctttctacaa gcagctgccc 780  
 caggacctgg ggacggctta ctacctcacc tcccaggcca tgggtggacaa cctggccctg 840  
 cgggacgggc aggagggcat cacggccttc ctccagaaga gaaaacctgt ctggtcacac 900  
 gagccagtgt ga 912

<210> 31  
 <211> 176  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Ala Val Ile Lys Leu Asp Arg Pro Glu Glu Ala Val Asn Ala Leu Ser  
 1 5 10 15  
 Ala Glu Leu Leu Thr Glu Leu Ile Glu Ala Leu Glu Lys Leu Glu Gln  
 20 25 30  
 Asp Pro Ser Val Arg Ala Val Val Leu Thr Gly Ala Gly Pro Gly Ala  
 35 40 45  
 Phe Ser Ala Gly Ala Asp Ile Lys Glu Met Ala Ala Gly Phe Lys Glu  
 50 55 60  
 Pro Leu Ala Glu Gln Ala Gln Phe Ser Leu Glu Ala Gln Asp Leu Trp  
 65 70 75 80  
 Ser Lys Leu Glu Asp Leu Pro Lys Pro Val Ile Ala Ala Val Asn Gly  
 85 90 95  
 Tyr Ala Leu Gly Gly Gly Leu Glu Leu Ala Leu Ala Cys Asp Tyr Arg  
 100 105 110  
 Ile Ala Ala Asp Asn Ala Lys Tyr Val Phe Gly Leu Pro Glu Val Lys  
 115 120 125  
 Leu Gly Ile Ile Pro Gly Ala Gly Gly Thr Gln Arg Leu Pro Arg Ile  
 130 135 140  
 Val Gly Val Ser Ala Ala Leu Glu Met Ile Leu Thr Gly Arg Arg Ile  
 145 150 155 160  
 Arg Ala Gln Glu Ala Leu Lys Met Gly Leu Val Asp Lys Val Val Pro  
 165 170 175